

ID 053651 PRELIMINARY: PRT: 255 AA.  
AC 053651:  
DT 01-NOV-1996 (TREMblrel: 01, Created)  
DT 01-NOV-1996 (TREMblrel: 01, Last sequence update)  
DE CAMP FACTOR PRECURSOR.  
OS Streptococcus agalactiae.  
OC Bacteria: Firmicutes: Bacillus/Clostridium group: Streptococcaceae;  
OC Streptococcus.  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN-R268:  
RA MEDLINE: 95231384.  
\* POBBIESTRI A.:  
RT "Molecular characterization of the cfb gene encoding group B  
streptococcal CAMP-factor."  
RL Med. Microbiol. Immunol. 183:239-256(1994).  
DR EMBL: X72754; CAA51283.1; .  
PT SIGNAL.  
.. MAIN 1 26 POTENTIAL.  
SQ SEQUENCE 255 AA: 28373 MW: 5938126E CRC32:

Query Match 53.5%: Score 794.5; DB 2: Length 255;  
Best Local Similarity 63.0%: Pred. No. 1.2e+43;  
Matches 155: Conservative 37: Mismatches 47: Indels 13: Gaps 3:

UY 1 MEKFLLYTOS-1AGTILFSPILTSVQANQINVSOP-----PSNSESINYSCKEIDNS 54  
DB 1 MNVTHMYLGLTIGVAGLLEFSPAVLEHNDQVTPGVVHVNNSNNOAQOMAK----- 54  
UY 55 LNOESQALYALKEVDVGTETECSEVNSAISEVENKTSLSAANEETIYDLSICIRFEAISD 114  
DB 54 LDDSDIOLRNKIKONVQGTDEKPVNENAIISVEKLTSLRANPEIYVDINSISREVALTD 113  
UY 115 VIGAIYFSTOOLINKVQADHLEMGFAIKLIRADPFASNSISGVEAVYQVATVLT 174  
DB 114 VIBATFSTOHLTNKVSQANIDMGFGITKLVIRIDPFASVSIKAQVNDVVALEQKVL 173  
UY 175 YPDLPTDRATITVVKSKLKLIMQTRITRDQVYLVNKSFEVYHOLNKAITHAVQVQLNPT 234  
DB 174 YPDLKPTDRATITVVKSKLKLIMQTRITRDQVYLVNKSFEVYHOLNKAITHAVQVQLNPT 233  
UY 235 VTVAQVDEIKVLOEALNTAQ 256  
DB 234 VTVAQVDEIKVLOEALNTAQ 255  
Res3  
ID 086016 PRELIMINARY: PRT: 257 AA.  
AC 086016:  
DT 01-NOV-1998 (TREMblrel: 08, Created)  
DT 01-NOV-1998 (TREMblrel: 08, Last sequence update)  
DE CAMP FACTOR.  
GN CFA.  
OS Streptococcus pyogenes.  
OC Bacteria: Firmicutes: Bacillus/Clostridium group: Streptococcaceae;  
OC Streptococcus.  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN-SF370:  
RA GAGE K., MCSHAN W.M., PRIMEAUX C., FERRETTI J.J.:  
RT "The CAMP factor gene (cfa) of group A streptococci: identification,  
cloning, and expression."  
RL Submitted (Jul-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF079302; AAC29481.1;  
SQ SEQUENCE 257 AA: 28480 MW: EC5BD8E3 CRC32:

Query Match 56.7%: Score 710: DB 2: Length 257;

Best Local Similarity 55.6%: Pred. No. 2.7e+38;  
Matches 145: Conservative 51: Mismatches 55: Indels 1:  
UY 1 MEKFLLYTOS-1AGTILFSPILTSVQANQINVSOP-----PSNSESINYSCKEIDNS 54  
DB 1 MKPKHLLSTVYAGLLEFSTMTSHVAD--DASNDALIMNNON 55  
UY 56 NQESQALYALKEVDVGTETECSEVNSAISEVENKTSLSAANEETIYDLSICIRFEAISD 114  
DB 56 DEHQOLEAIKHEAKGIDITETVKAIDAVIDHMKSSIRPENTETVD 113  
UY 116 IOAIVFSTOOLINKVQADHLEMGFAIKLIRADPFASNSISGVEAVYQVATVLT 174  
DB 116 IKAIYFSTOFTKVEKATDMQFALIKLVIRIDPFASVQATVLT 173  
UY 176 PDLOPTDRATITVVKSKLKLIMQTRITRDQVYLVNKSFEVYHOLNKAITHAVQVQLNPT 234  
DB 176 PDLOPTDRATITVVKSKLKLIMQTRITRDQVYLVNKSFEVYHOLNKAITHAVQVQLNPT 233  
UY 236 VTVAQVDEIKVLOEALNTAQ 256  
DB 236 VTVAQVDEIKVLOEALNTAQ 255

RESULT 4  
ID P78969 PRELIMINARY: PRT: 1526 AA.  
AC P78969:  
DT 01-MAY-1997 (TREMblrel: 03, Created)  
DT 01-MAY-1997 (TREMblrel: 03, Last sequence update)  
DE 01-MAY-1999 (TREMblrel: 10, Last annotation update)  
GN MYO2.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Arctiascomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomyces.  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN-972 H-1:  
RA MAY K.M., WATTS F.Z., JONES N., HYAMS J.S.:  
RL Mol. Biol. Cell 0:0-0(1996).  
RN (2)  
RP SEQUENCE FROM N.A.  
RC STRAIN-972 H-1:  
RX MEDLINE: 98075862.  
RA MAY K.M., WATTS F.Z., JONES N., HYAMS J.S.:  
RT "Type II myosin involved in cytokinesis in the fss-1  
Schizosaccharomyces pombe."  
RL Cell Motil. Cytoskeleton 38:385-396(1997).  
DR EMBL: U75357; AAC49908.1; .  
DR PFAM: PF00612; IO: 1.  
DR PFAM: PF00612; myosin-head; .  
SQ SEQUENCE 1526 AA: 176499 MW: 10AF564F CRC32:

Query Match 9.3%: Score 116.5; DB 3: Length 257;  
Best Local Similarity 20.9%: Pred. No. 11;  
Matches 51: Conservative 61: Mismatches 83: Indels 1:

UY 52 DNSLNQESQALYALKEVDVGTETECSEVNSAISEVENKTSLSAANEETIYDLSICIRFEAISD 114  
DB 823 DKOLKRDADIELKELKQONKSEVERDLVETNSLAVENLLT 113  
UY 93 RANPETIYDLSIGTRVREALSDVIAIVFSTOOLINKVQADHLEMGFAIKLIRADPFASNSISGVEAVYQVATVLT 174  
DB 883 PRTOERLANIEDSFSEKCONENKRESASLKOINNELESELENTS- 173  
UY 150 DPFASNE-----SIKQVEAVYQVATVLT-----YPDLPTDRATITVVKSKLKLIMQTRITRDQVYLVNKSFEVYHOLNKAITHAVQVQLNPT 234  
DB 943 EKLSLEKDLDTKGELESIRENNATVLSKAEFNEQCKSIOETIVT 233  
UY 196 -----IMQTRITRDQVYLVNKSFEVYHOLNKAITHAVQVQLNPT 233



|                        |              |                |      |             |
|------------------------|--------------|----------------|------|-------------|
| Empty Match:           | 27.56        | Score 3374     | DB 1 | Length 1457 |
| Best Local Similarity: | 64.96        | Prod. No. 3e37 |      |             |
| Matches 526            | Conservative |                |      |             |

Db 998 TGCATCCAAATCTTACGCGA TAAATATGATCAAGATCTT  
 907 TTAATACCTGCTCTTACATATCTGAAATTT 997  
 Db 1058 CTCATACAGCATTTAAATTTAAATTTTATTTTCTT 1057

| RESULT     | 3                           |
|------------|-----------------------------|
| AF079502   |                             |
| LOCUS      | AF079402                    |
| DEFINITION | Streptococcus faecalis 3264 |
| ACCESSION  | AF079502                    |
| NID        | 93406758                    |
| VERSION    | AF079502.1                  |
| KEYWORDS   |                             |
| SOURCE     | Streptococcus               |

ORGANISM  
*Streptococcus faecalis*  
*Streptococcus faecalis*  
Bacteria: Firmicutes: Bacillus/*Streptococcus*  
Streptococcaceae  
1 (bases) 1 to 2000  
Gase, K., Meislin, W.M., Lindebaum, J., and Ford,  
The CAMP factor (CAMP) of group A strep-  
tococci, and expression  
cloning, and expression  
2 (bases) 1 to 2000  
Gase, K., Meislin, W.M., Lindebaum, J., and Ford,  
Direct Submission  
Submitted (21 JUL 1998) Microbiology and  
Oklahoma Health Sciences Center, 940 S.W. 10th  
City, OK 73109, USA

| FEATURES           | source      |
|--------------------|-------------|
| Location/addresses | 1. 2. 3. 4. |

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/OTM:gene="ZNF600.CCDS_77398.1"
/submitter="NCBI"
/chxref="NM_021837.3"
787..756
/gene="CDK"
787..751

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[illegible]

|                       |                   |                  |
|-----------------------|-------------------|------------------|
| Query Match           | 25.00             | Score 309; 36    |
| Best Local Similarity | 59.76             | Precl. No. 36.34 |
| Matches               | 555; Conservative | Matches          |

QY 32 TATTTTATGATAATTAATAATTTTAACTATAAAAATTTTAT  
|||||  
EB 657 TATTTTCTGAAATTAATAATAATCTAGCTATAAAAAATAAAT  
|||||  
QY 92 TAACTACTTATTTATTTATATATGCAAT-----TATAAATA  
|||||  
Db 717 TAAAGCTTTAAATTAATTAAGTCTACTTAAGTATTTAAATAG  
|||||  
QY 147 AGGATGCTTATGGAATTAATAATTTCTTATTTAACTATTTGA  
|||||  
Db 777 GAGCAATTAATATGAAAGCAAAACACTCTCTCTCTTCAATAGT  
|||||  
QY 207 TTTATTTTCCCAATTTTAAATAATCTAGAGAAATTAATAAAT  
|||||  
Db 837 TTTATTTTCAACTATATAGCAATTAATTAATTTAGCTATGATATTTGA  
|||||